Claims

We claim:

1. A polynucleotide encoding a mutant starch biosynthesis protein, or a biologically-active fragment or variant of said mutant protein, wherein said mutant protein exhibits increased heat stability relative to the wild type protein.

2. The polynucleotide according to claim 1, wherein said mutant protein encoded by said polynucleotide is a plant AGP protein.

3. The polynucleotide according to claim 2, wherein said mutant protein encoded by said polynucleotide comprises an amino acid mutation in the large subunit of said protein.

4. The polynucleotide according to claim 2, wherein said mutant protein encoded by said polynucleotide comprises an amino acid mutation in the small subunit of said protein.

5. The polynucleotide according to claim 3, wherein said mutant protein encoded by said polynucleotide comprises an amino acid mutation wherein a histidine residue at position 333 in the amino acid sequence of said protein is replaced by an amino acid that confers heat stability to said protein.

6. The polynucleotide according to claim 5, wherein said amino acid substituted for histidine at position number 333 is a glycine.

7. The polynucleotide according to claim 5, wherein said amino acid substituted for histidine at position number 333 is a phenylalanine.

8. The polynucleotide according to claim 5, wherein said amino acid substituted for histidine at position number 333 is a methionine.

9. The polynucleotide according to claim 1, wherein said mutant protein encoded by said polynucleotide further comprises an amino acid mutation that confers increased seed weight to a plant expressing said polynucleotide.

10. The polynucleotide according to claim 9, wherein said polynucleotide comprises the *Rev6* mutation.

11. The polynucleotide according to claim 9, wherein said polynucleotide encodes a maize large subunit AGP enzyme wherein at least one serine residue is inserted between amino acids 494 and 495 of the native AGP enzyme subunit.

12. The polynucleotide according to claim 9, wherein said polynucleotide encodes a maize large subunit AGP enzyme wherein the amino acid pair tyrosine:serine is inserted between amino acids 494 and 495 of the native AGP enzyme subunit.

13. The polynucleotide according to claim 9, wherein said polynucleotide encodes a maize large subunit AGP enzyme wherein the amino acid pair serine:tyrosine is inserted between amino acids 495 and 496 of the native AGP enzyme subunit.

14. A method for increasing resistance of a plant to heat stress conditions, said method comprising incorporating the polynucleotide of claim 1 into the genome of said plant and expressing the protein encoded by said polynucleotide molecule.

15. The method according to claim 14, wherein said plant is a monocotyledonous plant.

16. The method according to claim 15, wherein said monocotyledonous plant is selected from the group consisting of rice, wheat, barley, oats, sorghum, maize, lilies, and millet.

17. The method according to claim 14, wherein said plant is *Zea mays*.

18. The method according to claim 14, wherein said plant is a dicotyledonous plant.

19. The method according to claim 18, wherein said dicotyledonous plant is selected from the group consisting of peas, alfalfa, chickpea, chicory, clover, kale, lentil, prairie grass, soybean, tobacco, potato, sweet potato, radish, cabbage, rape, apple trees, and lettuce.

20. A plant or plant tissue comprising the polynucleotide molecule of claim 1.

21. The plant or plant tissue according to claim 20, wherein said plant or plant tissue is monocotyledonous.

22. The plant or plant tissue according to claim 21, wherein said monocotyledonous plant or plant tissue is selected from the group consisting of rice, wheat, barley, oats, sorghum, maize, lilies, and millet.

23. The plant or plant tissue according to claim 20, wherein said plant is *Zea mays* or said plant tissue is from *Zea mays*.

24. The plant or plant tissue according to claim 20, wherein said plant or plant tissue is dicotyledonous.

25. The plant or plant tissue according to claim 24, wherein said dicotyledonous plant or plant tissue is selected from the group consisting of peas, alfalfa, chickpea, chicory, clover, kale, lentil, prairie grass, soybean, tobacco, potato, sweet potato, radish, cabbage, rape, apple trees, and lettuce.

26. The plant tissue according to claim 20, wherein said plant tissue is a seed.

27. A mutant starch biosynthesis protein encoded by the polynucleotide of claim 1.

28. A method for identifying a polynucleotide encoding a mutant starch biosynthesis protein wherein said mutant starch biosynthesis protein exhibits increased heat stability relative to a wild type protein, said method comprising mutating a polynucleotide encoding a starch biosynthesis protein, expressing said mutated polynucleotide in a cell to produce a mutant starch biosynthesis protein, and determining whether said mutant starch biosynthesis protein exhibits increased heat stability relative to the wild type starch biosynthesis protein.

29. A method for increasing a characteristic of a plant selected from the group consisting of seed number, plant biomass, Harvest Index, flag leaf weight, seed heads, and total seed weight, said method comprising incorporating the polynucleotide of claim 10 into the genome of said plant and expressing the protein encoded by said polynucleotide molecule.